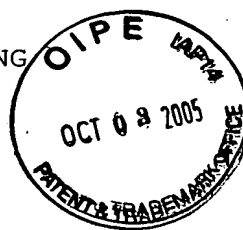


SEQUENCE LISTING



<110> Tuschl, Thomas
Martinez, Javier
Patkaniowska, Agnieszka
Urlaub, Henning
Luehrmann, Reinhard

<120> RNA-Interference by Single-Stranded RNA Molecules

<130> 2923-673

<140> 10/520,470

<141> 2005-01-07

<150> EP 02015532.1

<151> 2002-07-10

<150> EP 02018906.4

<151> 2002-08-23

<150> PCT/EP03/007516

<151> 2003-07-10

<160> 115

<170> PatentIn version 3.3

<210> 1

<211> 15

<212> RNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> HeLa S100

antisense siRNA (5'-3')

<400> 1

ucgaaguauu ccgcg

15

<210> 2

<211> 21

<212> RNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> HeLa S100

antisense siRNA (5'-3')

<400> 2

ucgaaguaau ccgcguacgu g

21

<210> 3
<211> 25
<212> RNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> HeLa S100
antisense siRNA (5'-3')

<400> 3
ucgaaguaau ccgcguacgu gaugu

25

<210> 4
<211> 27
<212> RNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> HeLa S100
antisense siRNA (5'-3')

<400> 4
ucgaaguaau ccgcguacgu gauguuc

27

<210> 5
<211> 29
<212> RNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> HeLa S100
antisense siRNA (5'-3')

<400> 5
ucgaaguaau ccgcguacgu gauguucac

29

<210> 6
<211> 15
<212> RNA
<213> Homo sapiens

<220>

<221> misc_feature
<223> HeLa S100
antisense siRNA (5'-3')

<400> 6
ucgaaguauu ccgcg

15

<210> 7
<211> 21
<212> RNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> HeLa S100
antisense siRNA (5'-3')

<400> 7
ucgaaguauu ccgcguacgu g

21

<210> 8
<211> 25
<212> RNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> HeLa S100
antisense siRNA (5'-3')

<400> 8
ucgaaguauu ccgcguacgu gaugu

25

<210> 9
<211> 27
<212> RNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> HeLa S100
antisense siRNA (5'-3')

<400> 9
ucgaaguauu ccgcguacgu gauguuc

27

<210> 10
<211> 29

<212> RNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> HeLa S100
antisense siRNA (5'-3')

<400> 10
ucgaaguauu ccgcguacgu gauguucac

29

<210> 11
<211> 21
<212> RNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> HeLa S100
antisense siRNA (5'-3')

<400> 11
ucgaaguauu ccgcguacgu g

21

<210> 12
<211> 21
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(21)
<223> RNA/DNA hybrid

<220>
<221> misc_feature
<223> HeLa S100
antisense siRNA (5'-3')

<220>
<221> misc_feature
<222> (20)..(20)
<223> n = 2'-deoxythymidine

<220>
<221> misc_feature
<222> (21)..(21)
<223> n = 2'-deoxyguanosine

<400> 12

ucgaaguauu ccgcguacgn n

21

<210> 13
<211> 21
<212> RNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> HeLa S100
antisense siRNA (5'-3')

<400> 13
ucgaaguauu ccgcguacgu u

21

<210> 14
<211> 21
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(21)
<223> RNA/DNA hybrid

<220>
<221> misc_feature
<223> HeLa S100
antisense siRNA (5'-3')

<220>
<221> misc_feature
<222> (20)..(21)
<223> n = 2'-deoxythymidine

<400> 14
ucgaaguauu ccgcguacgn n

21

<210> 15
<211> 21
<212> RNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> HeLa S100
antisense siRNA (5'-3')

<400> 15

ucgaaguaau ccgcguacgu g

21

<210> 16
<211> 21
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(21)
<223> RNA/DNA hybrid

<220>
<221> misc_feature
<223> HeLa S100 cells
antisense siRNA (5'-3')

<220>
<221> misc_feature
<222> (20)..(20)
<223> n = 2'-deoxythymidine

<220>
<221> misc_feature
<222> (21)..(21)
<223> n = 2'-deoxyguanosine

<400> 16
ucgaaguaau ccgcguacgn n

21

<210> 17
<211> 21
<212> RNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> HeLa S100
antisense siRNA (5'-3')

<400> 17
ucgaaguaau ccgcguacgu u

21

<210> 18
<211> 21
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (1)..(21)
<223> RNA/DNA hybrid

<220>
<221> misc_feature
<223> HeLa S100
antisense siRNA (5'-3')

<220>
<221> misc_feature
<222> (20)..(21)
<223> n = 2'-deoxythymidine

<400> 18
ucgaaguauu ccgcguacgn n

21

<210> 19
<211> 21
<212> RNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> HeLa S100
sense siRNA (5'-3')

<400> 19
cguacgcgga auacuucgaa a

21

<210> 20
<211> 21
<212> RNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> HeLa S100
antisense siRNA (5'-3')

<400> 20
ucgaaguauu ccgcguacgu g

21

<210> 21
<211> 21
<212> RNA
<213> Homo sapiens

<220>

<221> misc_feature
<223> HeLa S100
sense siRNA (5'-3')

<400> 21
cguacgcgga auacuucgaa a

21

<210> 22
<211> 21
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(21)
<223> RNA/DNA hybrid

<220>
<221> misc_feature
<223> HeLa S100
antisense siRNA (5'-3')

<220>
<221> misc_feature
<222> (20)..(20)
<223> n = 2'-deoxythymidine

<220>
<221> misc_feature
<222> (21)..(21)
<223> n = 2'-deoxyguanosine

<400> 22
ucgaaguauu ccgcguacgn n

21

<210> 23
<211> 21
<212> RNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> HeLa S100
sense siRNA (5'-3')

<400> 23
cguacgcgga auacuucgaa a

21

<210> 24
<211> 21

<212> RNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> HeLa S100
antisense siRNA (5'-3')

<400> 24
ucgaaguaau ccgcguacgu u

21

<210> 25
<211> 21
<212> RNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> HeLa S100
sense siRNA (5'-3')

<400> 25
cguacgcgga auacuucgaa a

21

<210> 26
<211> 21
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(21)
<223> RNA/DNA hybrid

<220>
<221> misc_feature
<223> HeLa S100
antisense siRNA (5'-3')

<220>
<221> misc_feature
<222> (20)..(21)
<223> n = 2'-deoxythymidine

<400> 26
ucgaaguaau ccgcguacgn n

21

<210> 27
<211> 21

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(21)
<223> RNA/DNA hybrid

<220>
<221> misc_feature
<223> HeLa S100
antisense siRNA (5'-3')

<220>
<221> misc_feature
<222> (1)..(1)
<223> n = 2'-deoxythymidine

<400> 27
ncgaaguauu ccgcguacgu u

21

<210> 28
<211> 21
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(21)
<223> RNA/DNA hybrid

<220>
<221> misc_feature
<223> HeLa S100
sense siRNA (5'-3')

<220>
<221> misc_feature
<222> (1)..(1)
<223> n = 2'-deoxycytidine

<400> 28
nguacgcgga auacuucgau u

21

<210> 29
<211> 21
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (1)..(21)
<223> RNA/DNA hybrid

<220>
<221> misc_feature
<223> HeLa S100
antisense siRNA (5'-3')

<220>
<221> misc_feature
<222> (1)..(1)
<223> n = 2'-deoxythymidine

<400> 29
ncgaaguauu ccgcguacgu u

21

<210> 30
<211> 21
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(21)
<223> RNA/DNA hybrid

<220>
<221> misc_feature
<223> HeLa S100 cells
antisense siRNA (5'-3')

<220>
<221> misc_feature
<222> (1)..(21)
<223> n = 2'-deoxythymidine

<400> 30
ncgaaguauu ccgcguacgn n

21

<210> 31
<211> 21
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(21)
<223> RNA/DNA hybrid

<220>

<221> misc_feature
<223> HeLa S100
sense siRNA (5'-3')

<220>
<221> misc_feature
<222> (1)..(1)
<223> n = 2'-deoxycytidine

<220>
<221> misc_feature
<222> (20)..(21)
<223> n = 2'-deoxythymidine

<400> 31
nguacgcgga auacuucgan n

21

<210> 32
<211> 21
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(21)
<223> RNA/DNA hybrid

<220>
<221> misc_feature
<223> HeLa S100
antisense siRNA (5'-3')

<220>
<221> misc_feature
<222> (1)..(21)
<223> n = 2'-deoxythymidine

<400> 32
ncgaaguauu ccgcguacgn n

21

<210> 33
<211> 21
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(21)
<223> RNA/DNA hybrid

<220>

<221> misc_feature
<223> HeLa S100
antisense siRNA (5'-3')

<220>
<221> misc_feature
<222> (1)..(21)
<223> n = 2'-deoxythymidine

<400> 33
ncgaaguaau ccgcguacgn n

21

<210> 34
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> peptide fragment of HILI, corresponding to position 17-29 of the
protein

<400> 34

Asn Lys Gln Asp Phe Met Asp Leu Ser Ile Cys Thr Arg
1 5 10

<210> 35
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> peptide fragment of HILI, corresponding to position 436-449 of
the protein

<400> 35

Thr Glu Tyr Val Ala Glu Ser Phe Leu Asn Cys Leu Arg Arg
1 5 10

<210> 36
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE

<223> peptide fragment of HILI, corresponding to position 591-603 of the protein

<400> 36

Tyr Asn His Asp Leu Pro Ala Arg Ile Ile Val Tyr Arg
1 5 10

<210> 37

<211> 35

<212> RNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> HeLa S100

target RNA

<400> 37

aacaucacgu acgcggaaua cuucgaaaug uccgu

35

<210> 38

<211> 21

<212> RNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> HeLa S100

strand of siRNA duplex

<400> 38

cguacgcgga auacuucgau u

21

<210> 39

<211> 21

<212> RNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> HeLa S100

strand of siRNA duplex

<400> 39

ucgaaguauu ccgcguacgu u

21

<210> 40

<211> 21
<212> RNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> HeLa S100
strand of siRNA duplex

<400> 40
cguacgcgga auacuucgaa a

21

<210> 41
<211> 20
<212> RNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> HeLa S100
strand of siRNA duplex

<400> 41
ucgaaguauu ccgcguacgu

20

<210> 42
<211> 12
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> peptide fragment of eIF2C2, obtained by mass spectrometry

<400> 42

Val Leu Gln Pro Pro Ser Ile Leu Tyr Gly Gly Arg
1 5 10

<210> 43
<211> 12
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> peptide fragment of eIF2C2, obtained by mass spectrometry

<400> 43

Gln Glu Ile Ile Gln Asp Leu Ala Ala Met Val Arg
1 5 10

<210> 44

<211> 12

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> peptide fragment of eIF2C2, obtained by mass spectrometry

<400> 44

His Leu Pro Ser Met Arg Tyr Thr Pro Val Gly Arg
1 5 10

<210> 45

<211> 12

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> peptide fragment of eIF2C2, obtained by mass spectrometry

<400> 45

Lys Leu Thr Asp Asn Gln Thr Ser Thr Met Ile Arg
1 5 10

<210> 46

<211> 13

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> peptide fragment of eIF2C2, obtained by mass spectrometry

<400> 46

Tyr Ala Gln Gly Ala Asp Ser Val Glu Pro Met Phe Arg
1 5 10

<210> 47

<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> peptide fragment of eIF2C2, obtained by mass spectrometry

<400> 47

Asp Lys Val Glu Leu Glu Val Thr Leu Pro Gly Glu Gly Lys
1 5 10

<210> 48
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> peptide fragment of eIF2C2, obtained by mass spectrometry

<400> 48

Asp Ala Gly Met Pro Ile Gln Gly Gln Pro Cys Phe Cys Lys
1 5 10

<210> 49
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> peptide fragment of eIF2C2, obtained by mass spectrometry

<400> 49

Thr Gln Ile Phe Gly Asp Arg Lys Pro Val Phe Asp Gly Arg
1 5 10

<210> 50
<211> 15
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE

<223> peptide fragment of eIF2C2, obtained by mass spectrometry

<400> 50

Ala	Thr	Ala	Arg	Ser	Ala	Pro	Asp	Arg	Gln	Glu	Glu	Ile	Ser	Lys
1				5					10					15

<210> 51

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> peptide fragment of eIF2C2, obtained by mass spectrometry

<400> 51

Asp	Tyr	Gln	Pro	Gly	Ile	Thr	Phe	Ile	Val	Val	Gln	Lys	Arg
1				5					10				

<210> 52

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> peptide fragment of eIF2C2, obtained by mass spectrometry

<400> 52

Ser	Ala	Pro	Asp	Arg	Gln	Glu	Glu	Ile	Ser	Lys	Leu	Met	Arg
1				5					10				

<210> 53

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> peptide fragment of eIF2C2, obtained by mass spectrometry

<400> 53

Tyr	Pro	His	Leu	Pro	Cys	Leu	Gln	Val	Gly	Gln	Glu	Gln	Lys
1				5					10				

<210> 54
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> peptide fragment of eIF2C2, obtained by mass spectrometry
<400> 54

Ser Phe Phe Thr Ala Ser Glu Gly Cys Ser Asn Pro Leu Gly Gly Gly
1 5 10 15

Arg

<210> 55
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> peptide fragment of eIF2C2, obtained by mass spectrometry
<400> 55

Tyr His Leu Val Asp Lys Glu His Asp Ser Ala Glu Gly Ser His Thr
1 5 10 15

Ser Gly Gln Ser Asn Gly Arg
20

<210> 56
<211> 12
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> peptide fragment of eIF2C1, obtained by mass spectrometry
<400> 56

Val Leu Pro Ala Pro Ile Leu Gln Tyr Gly Gly Arg
1 5 10

<210> 57
<211> 12
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> peptide fragment of eIF2C1, obtained by mass spectrometry

<400> 57

Ser Val Ser Ile Pro Ala Pro Ala Tyr Tyr Ala Arg
1 5 10

<210> 58
<211> 12
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> peptide fragment of eIF2C1, obtained by mass spectrometry

<400> 58

Thr Ser Pro Gln Thr Leu Ser Asn Leu Cys Leu Lys
1 5 10

<210> 59
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> peptide fragment of eIF2C1, obtained by mass spectrometry

<400> 59

Tyr Ala Gln Gly Ala Asp Ser Val Glu Pro Met Phe Arg
1 5 10

<210> 60
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> peptide fragment of eIF2C1, obtained by mass spectrometry

<400> 60

Asn Ile Tyr Thr Val Thr Ala Leu Pro Ile Gly Asn Glu Arg
1 5 10

<210> 61
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> peptide fragment of eIF2C1, obtained by mass spectrometry

<400> 61

Val Asp Phe Glu Val Thr Ile Pro Gly Glu Gly Lys Asp Arg
1 5 10

<210> 62
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> HeLa S100 cells
peptide fragment of eIF2C1 obtained by mass spectrometry

<400> 62

Asp Ala Gly Met Pro Ile Gln Gly Gln Pro Cys Phe Cys Lys
1 5 10

<210> 63
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> peptide fragment of eIF2C1, obtained by mass spectrometry

<400> 63

Asn Ile Asp Glu Gln Pro Lys Pro Leu Thr Asp Ser Gln Arg
1 5 10

<210> 64
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> peptide fragment of eIF2C1, obtained by mass spectrometry

<400> 64

Ser Ala Pro Asp Arg Gln Glu Glu Ile Ser Arg Leu Met Lys
1 5 10

<210> 65
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> peptide fragment of eIF2C1, obtained by mass spectrometry

<400> 65

Asp Tyr Gln Pro Gly Ile Thr Tyr Ile Val Val Gln Lys Arg
1 5 10

<210> 66
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> peptide fragment of eIF2C1, obtained by mass spectrometry

<400> 66

Tyr Pro His Leu Pro Cys Leu Gln Val Gly Gln Glu Gln Lys
1 5 10

<210> 67
<211> 17

<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> peptide fragment of eIF2C1, obtained by mass spectrometry

<400> 67

Ser Phe Phe Ser Pro Pro Glu Gly Tyr Tyr His Pro Leu Gly Gly Gly
1 5 10 15

Arg

<210> 68
<211> 857
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> eIF2C1, predicted protein sequence

<400> 68

Met Glu Ala Gly Pro Ser Gly Ala Ala Ala Gly Ala Tyr Leu Pro Pro
1 5 10 15

Leu Gln Gln Val Phe Gln Ala Pro Arg Arg Pro Gly Ile Gly Thr Val
20 25 30

Gly Lys Pro Ile Lys Leu Leu Ala Asn Tyr Phe Glu Val Asp Ile Pro
35 40 45

Lys Ile Asp Val Tyr His Tyr Glu Val Asp Ile Lys Pro Asp Lys Cys
50 55 60

Pro Arg Arg Val Asn Arg Glu Val Val Glu Tyr Met Val Gln His Phe
65 70 75 80

Lys Pro Gln Ile Phe Gly Asp Arg Lys Pro Val Tyr Asp Gly Lys Lys
85 90 95

Asn Ile Tyr Thr Val Thr Ala Leu Pro Ile Gly Asn Glu Arg Val Asp

100

105

110

Phe Glu Val Thr Ile Pro Gly Glu Gly Lys Asp Arg Ile Phe Lys Val
 115 120 125

Ser Ile Lys Trp Leu Ala Ile Val Ser Trp Arg Met Leu His Glu Ala
 130 135 140

Leu Val Ser Gly Gln Ile Pro Val Pro Leu Glu Ser Val Gln Ala Leu
 145 150 155 160

Asp Val Ala Met Arg His Leu Ala Ser Met Arg Tyr Thr Pro Val Gly
 165 170 175

Arg Ser Phe Phe Ser Pro Pro Glu Gly Tyr Tyr His Pro Leu Gly Gly
 180 185 190

Gly Arg Glu Val Trp Phe Gly Phe His Gln Ser Val Arg Pro Ala Met
 195 200 205

Trp Lys Met Met Leu Asn Ile Asp Val Ser Ala Thr Ala Phe Tyr Lys
 210 215 220

Ala Gln Pro Val Ile Glu Phe Met Cys Glu Val Leu Asp Ile Arg Asn
 225 230 235 240

Ile Asp Glu Gln Pro Lys Pro Leu Thr Asp Ser Gln Arg Val Arg Phe
 245 250 255

Thr Lys Glu Ile Lys Gly Leu Lys Val Glu Val Thr His Cys Gly Gln
 260 265 270

Met Lys Arg Lys Tyr Arg Val Cys Asn Val Thr Arg Arg Pro Ala Ser
 275 280 285

His Gln Thr Phe Pro Leu Gln Leu Glu Ser Gly Gln Thr Val Glu Cys
 290 295 300

Thr Val Ala Gln Tyr Phe Lys Gln Lys Tyr Asn Leu Gln Leu Lys Tyr
 305 310 315 320

Pro His Leu Pro Cys Leu Gln Val Gly Gln Glu Gln Lys His Thr Tyr
 325 330 335

Leu Pro Leu Glu Val Cys Asn Ile Val Ala Gly Gln Arg Cys Ile Lys
 340 345 350

Lys Leu Thr Asp Asn Gln Thr Ser Thr Met Ile Lys Ala Thr Ala Arg
 355 360 365

Ser Ala Pro Asp Arg Gln Glu Glu Ile Ser Arg Leu Met Lys Asn Ala
 370 375 380

Ser Tyr Asn Leu Asp Pro Tyr Ile Gln Glu Phe Gly Ile Lys Val Lys
 385 390 395 400

Asp Asp Met Thr Glu Val Thr Gly Arg Val Leu Pro Ala Pro Ile Leu
 405 410 415

Gln Tyr Gly Gly Arg Asn Arg Ala Ile Ala Thr Pro Asn Gln Gly Val
 420 425 430

Trp Asp Met Arg Gly Lys Gln Phe Tyr Asn Gly Ile Glu Ile Lys Val
 435 440 445

Trp Ala Ile Ala Cys Phe Ala Pro Gln Lys Gln Cys Arg Glu Glu Val
 450 455 460

Leu Lys Asn Phe Thr Asp Gln Leu Arg Lys Ile Ser Lys Asp Ala Gly
 465 470 475 480

Met Pro Ile Gln Gly Gln Pro Cys Phe Cys Lys Tyr Ala Gln Gly Ala
 485 490 495

Asp Ser Val Glu Pro Met Phe Arg His Leu Lys Asn Thr Tyr Ser Gly
 500 505 510

Leu Gln Leu Ile Ile Val Ile Leu Pro Gly Lys Thr Pro Val Tyr Ala
 515 520 525

Glu Val Lys Arg Val Gly Asp Thr Leu Leu Gly Met Ala Thr Gln Cys
 530 535 540

Val Gln Val Lys Asn Val Val Lys Thr Ser Pro Gln Thr Leu Ser Asn
545 550 555 560

Leu Cys Leu Lys Ile Asn Val Lys Leu Gly Gly Ile Asn Asn Ile Leu
565 570 575

Val Pro His Gln Arg Ser Ala Val Phe Gln Gln Pro Val Ile Phe Leu
580 585 590

Gly Ala Asp Val Thr His Pro Pro Ala Gly Asp Gly Lys Lys Pro Ser
595 600 605

Ile Thr Ala Val Val Gly Ser Met Asp Ala His Pro Ser Arg Tyr Cys
610 615 620

Ala Thr Val Arg Val Gln Arg Pro Arg Gln Glu Ile Ile Glu Asp Leu
625 630 635 640

Ser Tyr Met Val Arg Glu Leu Leu Ile Gln Phe Tyr Lys Ser Thr Arg
645 650 655

Phe Lys Pro Thr Arg Ile Ile Phe Tyr Arg Asp Gly Val Pro Glu Gly
660 665 670

Gln Leu Pro Gln Ile Leu His Tyr Glu Leu Leu Ala Ile Arg Asp Ala
675 680 685

Cys Ile Lys Leu Glu Lys Asp Tyr Gln Pro Gly Ile Thr Tyr Ile Val
690 695 700

Val Gln Lys Arg His His Thr Arg Leu Phe Cys Ala Asp Lys Asn Glu
705 710 715 720

Arg Ile Gly Lys Ser Gly Asn Ile Pro Ala Gly Thr Thr Val Asp Thr
725 730 735

Asn Ile Thr His Pro Phe Glu Phe Asp Phe Tyr Leu Cys Ser His Ala
740 745 750

Gly Ile Gln Gly Thr Ser Arg Pro Ser His Tyr Tyr Val Leu Trp Asp
755 760 765

Asp Asn Arg Phe Thr Ala Asp Glu Leu Gln Ile Leu Thr Tyr Gln Leu
 770 775 780

Cys His Thr Tyr Val Arg Cys Thr Arg Ser Val Ser Ile Pro Ala Pro
 785 790 795 800

Ala Tyr Tyr Ala Arg Leu Val Ala Phe Arg Ala Arg Tyr His Leu Val
 805 810 815

Asp Lys Glu His Asp Ser Gly Glu Gly Ser His Ile Ser Gly Gln Ser
 820 825 830

Asn Gly Arg Asp Pro Gln Ala Leu Ala Lys Ala Val Gln Val His Gln
 835 840 845

Asp Thr Leu Arg Thr Met Tyr Phe Ala
 850 855

<210> 69
 <211> 860
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> eIF2C2, predicted protein sequence

<400> 69

Met Gly Val Leu Ser Ala Ile Pro Ala Leu Ala Pro Pro Ala Pro Pro
 1 5 10 15

Pro Pro Ile Gln Gly Tyr Ala Phe Lys Pro Pro Pro Arg Pro Asp Phe
 20 25 30

Gly Thr Ser Gly Arg Thr Ile Lys Leu Gln Ala Asn Phe Phe Glu Met
 35 40 45

Asp Ile Pro Lys Ile Asp Ile Tyr His Tyr Glu Leu Asp Ile Lys Pro
 50 55 60

Glu Lys Cys Pro Arg Arg Val Asn Arg Glu Ile Val Glu His Met Val

65

70

75

80

Gln His Phe Lys Thr Gln Ile Phe Gly Asp Arg Lys Pro Val Phe Asp
85 90 95

Gly Arg Lys Asn Leu Tyr Thr Ala Met Pro Leu Pro Ile Gly Arg Asp
100 105 110

Lys Val Glu Leu Glu Val Thr Leu Pro Gly Glu Gly Lys Asp Arg Ile
115 120 125

Phe Lys Val Ser Ile Lys Trp Val Ser Cys Val Ser Leu Gln Ala Leu
130 135 140

His Asp Ala Leu Ser Gly Arg Leu Pro Ser Val Pro Phe Glu Thr Ile
145 150 155 160

Gln Ala Leu Asp Val Val Met Arg His Leu Pro Ser Met Arg Tyr Thr
165 170 175

Pro Val Gly Arg Ser Phe Phe Thr Ala Ser Glu Gly Cys Ser Asn Pro
180 185 190

Leu Gly Gly Gly Arg Glu Val Trp Phe Gly Phe His Gln Ser Val Arg
195 200 205

Pro Ser Leu Trp Lys Met Met Leu Asn Ile Asp Val Ser Ala Thr Ala
210 215 220

Phe Tyr Lys Ala Gln Pro Val Ile Glu Phe Val Cys Glu Val Leu Asp
225 230 235 240

Phe Lys Ser Ile Glu Glu Gln Gln Lys Pro Leu Thr Asp Ser Gln Arg
245 250 255

Val Lys Phe Thr Lys Glu Ile Lys Gly Leu Lys Val Glu Ile Thr His
260 265 270

Cys Gly Gln Met Lys Arg Lys Tyr Arg Val Cys Asn Val Thr Arg Arg
275 280 285

Pro Ala Ser His Gln Thr Phe Pro Leu Gln Gln Glu Ser Gly Gln Thr
 290 295 300

Val Glu Cys Thr Val Ala Gln Tyr Phe Lys Asp Arg His Lys Leu Val
 305 310 315 320

Leu Arg Tyr Pro His Leu Pro Cys Leu Gln Val Gly Gln Glu Gln Lys
 325 330 335

His Thr Tyr Leu Pro Leu Glu Val Cys Asn Ile Val Ala Gly Gln Arg
 340 345 350

Cys Ile Lys Lys Leu Thr Asp Asn Gln Thr Ser Thr Met Ile Arg Ala
 355 360 365

Thr Ala Arg Ser Ala Pro Asp Arg Gln Glu Glu Ile Ser Lys Leu Met
 370 375 380

Arg Ser Ala Ser Phe Asn Thr Asp Pro Tyr Val Arg Glu Phe Gly Ile
 385 390 395 400

Met Val Lys Asp Glu Met Thr Asp Val Thr Gly Arg Val Leu Gln Pro
 405 410 415

Pro Ser Ile Leu Tyr Gly Gly Arg Asn Lys Ala Ile Ala Thr Pro Val
 420 425 430

Gln Gly Val Trp Asp Met Arg Asn Lys Gln Phe His Thr Gly Ile Glu
 435 440 445

Ile Lys Val Trp Ala Ile Ala Cys Phe Ala Pro Gln Arg Gln Cys Thr
 450 455 460

Glu Val His Leu Lys Ser Phe Thr Glu Gln Leu Arg Lys Ile Ser Arg
 465 470 475 480

Asp Ala Gly Met Pro Ile Gln Gly Gln Pro Cys Phe Cys Lys Tyr Ala
 485 490 495

Gln Gly Ala Asp Ser Val Glu Pro Met Phe Arg His Leu Lys Asn Thr
 500 505 510

Tyr Ala Gly Leu Gln Leu Val Val Val Ile Leu Pro Gly Lys Thr Pro
515 520 525

Val Tyr Ala Glu Val Lys Arg Val Gly Asp Thr Val Leu Gly Met Ala
530 535 540

Thr Gln Cys Val Gln Met Lys Asn Val Gln Arg Thr Thr Pro Gln Thr
545 550 555 560

Leu Ser Asn Leu Cys Leu Lys Ile Asn Val Lys Leu Gly Gly Val Asn
565 570 575

Asn Ile Leu Leu Pro Gln Gly Arg Pro Pro Val Phe Gln Gln Pro Val
580 585 590

Ile Phe Leu Gly Ala Asp Val Thr His Pro Pro Ala Gly Asp Gly Lys
595 600 605

Lys Pro Ser Ile Ala Ala Val Val Gly Ser Met Asp Ala His Pro Asn
610 615 620

Arg Tyr Cys Ala Thr Val Arg Val Gln Gln His Arg Gln Glu Ile Ile
625 630 635 640

Gln Asp Leu Ala Ala Met Val Arg Glu Leu Leu Ile Gln Phe Tyr Lys
645 650 655

Ser Thr Arg Phe Lys Pro Thr Arg Ile Ile Phe Tyr Arg Asp Gly Val
660 665 670

Ser Glu Gly Gln Phe Gln Gln Val Leu His His Glu Leu Leu Ala Ile
675 680 685

Arg Glu Ala Cys Ile Lys Leu Glu Lys Asp Tyr Gln Pro Gly Ile Thr
690 695 700

Phe Ile Val Val Gln Lys Arg His His Thr Arg Leu Phe Cys Thr Asp
705 710 715 720

Lys Asn Glu Arg Val Gly Lys Ser Gly Asn Ile Pro Ala Gly Thr Thr
725 730 735

Val Asp Thr Lys Ile Thr His Pro Thr Glu Phe Asp Phe Tyr Leu Cys
740 745 750

Ser His Ala Gly Ile Gln Gly Thr Ser Arg Pro Ser His Tyr His Val
755 760 765

Leu Trp Asp Asp Asn Arg Phe Ser Ser Asp Glu Leu Gln Ile Leu Thr
770 775 780

Tyr Gln Leu Cys His Thr Tyr Val Arg Cys Thr Arg Ser Val Ser Ile
785 790 795 800

Pro Ala Pro Ala Tyr Tyr Ala His Leu Val Ala Phe Arg Ala Arg Tyr
805 810 815

His Leu Val Asp Lys Glu His Asp Ser Ala Glu Gly Ser His Thr Ser
820 825 830

Gly Gln Ser Asn Gly Arg Asp His Gln Ala Leu Ala Lys Ala Val Gln
835 840 845

Val His Gln Asp Thr Leu Arg Thr Met Tyr Phe Ala
850 855 860

<210> 70
<211> 924
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> eIF2C3, predicted protein sequence

<400> 70

Ser Arg Ser Arg Val Pro Val Pro Gly Pro Gly Ala Ala Ala Ala Pro
1 5 10 15

Cys Pro Ala Pro Ala Ser Pro Arg Arg His Pro Ser Ala Asn Ile Pro
20 25 30

Glu Ile Lys Arg Tyr Ala Ala Ala Ala Ala Ala Ala Gly Pro Gly

35

40

45

Ala Gly Gly Ala Gly Asp Arg Gly Glu Ala Ala Pro Ala Ala Ala Met
50 55 60

Glu Ala Leu Gly Pro Gly Pro Pro Ala Ser Leu Phe Gln Pro Pro Arg
65 70 75 80

Arg Pro Gly Leu Gly Thr Val Gly Lys Pro Ile Arg Leu Leu Ala Asn
85 90 95

His Phe Gln Val Gln Ile Pro Lys Ile Asp Val Tyr His Tyr Asp Val
100 105 110

Asp Ile Lys Pro Glu Lys Arg Pro Arg Arg Val Asn Arg Glu Val Val
115 120 125

Asp Thr Met Val Arg His Phe Lys Met Gln Ile Phe Gly Asp Arg Gln
130 135 140

Pro Gly Tyr Asp Gly Lys Arg Asn Met Tyr Thr Ala His Pro Leu Pro
145 150 155 160

Ile Gly Arg Asp Arg Val Asp Met Glu Val Thr Leu Pro Gly Glu Gly
165 170 175

Lys Asp Gln Thr Phe Lys Val Ser Val Gln Trp Val Ser Val Val Ser
180 185 190

Leu Gln Leu Leu Leu Glu Ala Leu Ala Gly His Leu Asn Glu Val Pro
195 200 205

Asp Asp Ser Val Gln Ala Leu Asp Val Ile Thr Arg His Leu Pro Ser
210 215 220

Met Arg Tyr Thr Pro Val Gly Arg Ser Phe Phe Ser Pro Pro Glu Gly
225 230 235 240

Tyr Tyr His Pro Leu Gly Gly Gly Arg Glu Val Trp Phe Gly Phe His
245 250 255

Gln Ser Val Arg Pro Ala Met Trp Asn Met Met Leu Asn Ile Asp Val
 260 265 270

Ser Ala Thr Ala Phe Tyr Arg Ala Gln Pro Ile Ile Glu Phe Met Cys
 275 280 285

Glu Val Leu Asp Ile Gln Asn Ile Asn Glu Gln Thr Lys Pro Leu Thr
 290 295 300

Asp Ser Gln Arg Val Lys Phe Thr Lys Glu Ile Arg Gly Leu Lys Val
 305 310 315 320

Glu Val Thr His Cys Gly Gln Met Lys Arg Lys Tyr Arg Val Cys Asn
 325 330 335

Val Thr Arg Arg Pro Ala Ser His Gln Thr Phe Pro Leu Gln Leu Glu
 340 345 350

Asn Gly Gln Ala Met Glu Cys Thr Val Ala Gln Tyr Phe Lys Gln Lys
 355 360 365

Tyr Ser Leu Gln Leu Lys Tyr Pro His Leu Pro Cys Leu Gln Val Gly
 370 375 380

Gln Glu Gln Lys His Thr Tyr Leu Pro Leu Glu Val Cys Asn Ile Val
 385 390 395 400

Ala Gly Gln Arg Cys Ile Lys Lys Leu Thr Asp Asn Gln Thr Ser Thr
 405 410 415

Met Ile Lys Ala Thr Ala Arg Ser Ala Pro Asp Arg Gln Glu Glu Ile
 420 425 430

Ser Arg Leu Val Lys Ser Asn Ser Met Val Gly Gly Pro Asp Pro Tyr
 435 440 445

Leu Lys Glu Phe Gly Ile Val Val His Asn Glu Met Thr Glu Leu Thr
 450 455 460

Gly Arg Val Leu Pro Ala Pro Met Leu Gln Tyr Gly Gly Arg Asn Lys
 465 470 475 480

Thr	Val	Ala	Thr	Pro	Asn	Gln	Gly	Val	Trp	Asp	Met	Arg	Gly	Lys	Gln	485	490	495
Phe	Tyr	Ala	Gly	Ile	Glu	Ile	Lys	Val	Trp	Ala	Val	Ala	Cys	Phe	Ala	500	505	510
Pro	Gln	Lys	Gln	Cys	Arg	Glu	Asp	Leu	Leu	Lys	Ser	Phe	Thr	Asp	Gln	515	520	525
Leu	Arg	Lys	Ile	Ser	Lys	Asp	Ala	Gly	Met	Pro	Ile	Gln	Gly	Gln	Pro	530	535	540
Cys	Phe	Cys	Lys	Tyr	Ala	Gln	Gly	Ala	Asp	Ser	Val	Glu	Pro	Met	Phe	545	550	555
Lys	His	Leu	Lys	Met	Thr	Tyr	Val	Gly	Leu	Gln	Leu	Ile	Val	Val	Ile	565	570	575
Leu	Pro	Gly	Lys	Thr	Pro	Val	Tyr	Ala	Glu	Val	Lys	Arg	Val	Gly	Asp	580	585	590
Thr	Leu	Leu	Gly	Met	Ala	Thr	Gln	Cys	Val	Gln	Val	Lys	Asn	Val	Val	595	600	605
Lys	Thr	Ser	Pro	Gln	Thr	Leu	Ser	Asn	Leu	Cys	Leu	Lys	Ile	Asn	Ala	610	615	620
Lys	Leu	Gly	Gly	Ile	Asn	Asn	Val	Leu	Val	Pro	His	Gln	Arg	Pro	Ser	625	630	635
Val	Phe	Gln	Gln	Pro	Val	Ile	Phe	Leu	Gly	Ala	Asp	Val	Thr	His	Pro	645	650	655
Pro	Ala	Gly	Asp	Gly	Lys	Lys	Pro	Ser	Ile	Ala	Ala	Val	Val	Gly	Ser	660	665	670
Met	Asp	Gly	His	Pro	Ser	Arg	Tyr	Cys	Ala	Thr	Val	Arg	Val	Gln	Thr	675	680	685
Ser	Arg	Gln	Glu	Ile	Ser	Gln	Glu	Leu	Leu	Tyr	Ser	Gln	Glu	Val	Ile	690	695	700

Gln Asp Leu Thr Asn Met Val Arg Glu Leu Leu Ile Gln Phe Tyr Lys
705 710 715 720

Ser Thr Arg Phe Lys Pro Thr Arg Ile Ile Tyr Tyr Arg Gly Gly Val
725 730 735

Ser Glu Gly Gln Met Lys Gln Val Ala Trp Pro Glu Leu Ile Ala Ile
740 745 750

Arg Lys Ala Cys Ile Ser Leu Glu Glu Asp Tyr Arg Pro Gly Ile Thr
755 760 765

Tyr Ile Val Val Gln Lys Arg His His Thr Arg Leu Phe Cys Ala Asp
770 775 780

Lys Thr Glu Arg Val Gly Lys Ser Gly Asn Val Pro Ala Gly Thr Thr
785 790 795 800

Val Asp Ser Thr Ile Thr His Pro Ser Glu Phe Asp Phe Tyr Leu Cys
805 810 815

Ser His Ala Gly Ile Gln Gly Thr Ser Arg Pro Ser His Tyr Gln Val
820 825 830

Leu Trp Asp Asp Asn Cys Phe Thr Ala Asp Glu Leu Gln Leu Leu Thr
835 840 845

Tyr Gln Leu Cys His Thr Tyr Val Arg Cys Thr Arg Ser Val Ser Ile
850 855 860

Pro Ala Pro Ala Tyr Tyr Ala Arg Leu Val Ala Phe Arg Ala Arg Tyr
865 870 875 880

His Leu Val Asp Lys Asp His Asp Ser Ala Glu Gly Ser His Val Ser
885 890 895

Gly Gln Ser Asn Gly Arg Asp Pro Gln Ala Leu Ala Lys Ala Val Gln
900 905 910

Ile His His Asp Thr Gln His Thr Met Tyr Phe Ala

<210> 71
 <211> 855
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> eIF2C4, predicted protein sequence

<400> 71

Ala Gly Pro Ala Gly Ala Gln Pro Leu Leu Met Val Pro Arg Arg Pro
 1 5 10 15

Gly Tyr Gly Thr Met Gly Lys Pro Ile Lys Leu Leu Ala Asn Cys Phe
 20 25 30

Gln Val Glu Ile Pro Lys Ile Asp Val Tyr Leu Tyr Glu Val Asp Ile
 35 40 45

Lys Pro Asp Lys Cys Pro Arg Arg Val Asn Arg Glu Val Val Asp Ser
 50 55 60

Met Val Gln His Phe Lys Val Thr Ile Phe Gly Asp Arg Arg Pro Val
 65 70 75 80

Tyr Asp Gly Lys Arg Ser Leu Tyr Thr Ala Asn Pro Leu Pro Val Ala
 85 90 95

Thr Thr Gly Val Asp Leu Asp Val Thr Leu Pro Gly Glu Gly Gly Lys
 100 105 110

Asp Arg Pro Phe Lys Val Ser Ile Lys Phe Val Ser Arg Val Ser Trp
 115 120 125

His Leu Leu His Glu Val Leu Thr Gly Arg Thr Leu Pro Glu Pro Leu
 130 135 140

Glu Leu Asp Lys Pro Ile Ser Thr Asn Pro Val His Ala Val Asp Val
 145 150 155 160

Val	Leu	Arg	His	Leu	Pro	Ser	Met	Lys	Tyr	Thr	Pro	Val	Gly	Arg	Ser	165	170	175
Phe	Phe	Ser	Ala	Pro	Glu	Gly	Tyr	Asp	His	Pro	Leu	Gly	Gly	Gly	Arg	180	185	190
Glu	Val	Trp	Phe	Gly	Phe	His	Gln	Ser	Val	Arg	Pro	Ala	Met	Trp	Lys	195	200	205
Met	Met	Leu	Asn	Ile	Asp	Val	Ser	Ala	Thr	Ala	Phe	Tyr	Lys	Ala	Gln	210	215	220
Pro	Val	Ile	Gln	Phe	Met	Cys	Glu	Val	Leu	Asp	Ile	His	Asn	Ile	Asp	225	230	235
Glu	Gln	Pro	Arg	Pro	Leu	Thr	Asp	Ser	His	Arg	Val	Lys	Phe	Thr	Lys	245	250	255
Glu	Ile	Lys	Gly	Leu	Lys	Val	Glu	Val	Thr	His	Cys	Gly	Thr	Met	Arg	260	265	270
Arg	Lys	Tyr	Arg	Val	Cys	Asn	Val	Thr	Arg	Arg	Pro	Ala	Ser	His	Gln	275	280	285
Thr	Phe	Pro	Leu	Gln	Leu	Glu	Asn	Gly	Gln	Thr	Val	Glu	Arg	Thr	Val	290	295	300
Ala	Gln	Tyr	Phe	Arg	Glu	Lys	Tyr	Thr	Leu	Gln	Leu	Lys	Tyr	Pro	His	305	310	315
Leu	Pro	Cys	Leu	Gln	Val	Gly	Gln	Glu	Gln	Lys	His	Thr	Tyr	Leu	Pro	325	330	335
Leu	Glu	Val	Cys	Asn	Ile	Val	Ala	Gly	Gln	Arg	Cys	Ile	Lys	Lys	Leu	340	345	350
Thr	Asp	Asn	Gln	Thr	Ser	Thr	Met	Ile	Lys	Ala	Thr	Ala	Arg	Ser	Ala	355	360	365
Pro	Asp	Arg	Gln	Glu	Glu	Ile	Ser	Arg	Leu	Val	Arg	Ser	Ala	Asn	Tyr	370	375	380

Glu Thr Asp Pro Phe Val Gln Glu Phe Gln Phe Lys Val Arg Asp Glu
 385 390 395 400

Met Ala His Val Thr Gly Arg Val Leu Pro Ala Pro Met Leu Gln Tyr
 405 410 415

Gly Gly Arg Asn Arg Thr Val Ala Thr Pro Ser His Gly Val Trp Asp
 420 425 430

Met Arg Gly Lys Gln Phe His Thr Gly Val Glu Ile Lys Met Trp Ala
 435 440 445

Ile Ala Cys Phe Ala Thr Gln Arg Gln Cys Arg Glu Glu Ile Leu Lys
 450 455 460

Gly Phe Thr Asp Gln Leu Arg Lys Ile Ser Lys Asp Ala Gly Met Pro
 465 470 475 480

Ile Gln Gly Gln Pro Cys Phe Cys Lys Tyr Ala Gln Gly Ala Asp Ser
 485 490 495

Val Glu Pro Met Phe Arg His Leu Lys Asn Thr Tyr Ser Gly Leu Gln
 500 505 510

Leu Ile Ile Val Ile Leu Pro Gly Lys Thr Pro Val Tyr Ala Glu Val
 515 520 525

Lys Arg Val Gly Asp Thr Leu Leu Gly Met Ala Thr Gln Cys Val Gln
 530 535 540

Val Lys Asn Val Ile Lys Thr Ser Pro Gln Thr Leu Ser Asn Leu Cys
 545 550 555 560

Leu Lys Ile Asn Val Lys Leu Gly Gly Ile Asn Asn Ile Leu Val Pro
 565 570 575

His Gln Arg Pro Ser Val Phe Gln Gln Pro Val Ile Phe Leu Gly Ala
 580 585 590

Asp Val Thr His Pro Pro Ala Gly Asp Gly Lys Lys Pro Ser Ile Ala
 595 600 605

Ala Val Val Gly Ser Met Asp Ala His Pro Ser Arg Tyr Cys Ala Thr
 610 615 620

Val Arg Val Gln Arg Pro Arg Gln Glu Ile Ile Gln Asp Leu Ala Ser
 625 630 635 640

Met Val Arg Glu Leu Leu Ile Gln Phe Tyr Lys Ser Thr Arg Phe Lys
 645 650 655

Pro Thr Arg Ile Ile Phe Tyr Arg Asp Gly Val Ser Glu Gly Gln Phe
 660 665 670

Arg Gln Val Leu Tyr Tyr Glu Leu Leu Ala Ile Arg Glu Ala Cys Ile
 675 680 685

Ser Leu Glu Lys Asp Tyr Gln Pro Gly Ile Thr Tyr Ile Val Val Gln
 690 695 700

Lys Arg His His Thr Arg Leu Phe Cys Ala Asp Arg Thr Glu Arg Val
 705 710 715 720

Gly Arg Ser Gly Asn Ile Pro Ala Gly Thr Thr Val Asp Thr Asp Ile
 725 730 735

Thr His Pro Tyr Glu Phe Asp Phe Tyr Leu Cys Ser His Ala Gly Ile
 740 745 750

Gln Gly Thr Ser Arg Pro Ser His Tyr His Val Leu Trp Asp Asp Asn
 755 760 765

Cys Phe Thr Ala Asp Glu Leu Gln Leu Leu Thr Tyr Gln Leu Cys His
 770 775 780

Thr Tyr Val Arg Cys Thr Arg Ser Val Ser Ile Pro Ala Pro Ala Tyr
 785 790 795 800

Tyr Ala His Leu Val Ala Phe Arg Ala Arg Tyr His Leu Val Asp Lys
 805 810 815

Glu His Asp Ser Ala Glu Gly Ser His Val Ser Gly Gln Ser Asn Gly

820

825

830

Arg Asp Pro Gln Ala Leu Ala Lys Ala Val Gln Ile His Gln Asp Thr
 835 840 845

Leu Arg Thr Met Tyr Phe Ala
 850 855

<210> 72
 <211> 764
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> HILI, predicted protein sequence

<400> 72

Ile Ser Ser Gly Asp Ala Gly Ser Thr Phe Met Glu Arg Gly Val Lys
 1 5 10 15

Asn Lys Gln Asp Phe Met Asp Leu Ser Ile Cys Thr Arg Glu Lys Leu
 20 25 30

Ala His Val Arg Asn Cys Lys Thr Gly Ser Ser Gly Ile Pro Val Lys
 35 40 45

Leu Val Thr Asn Leu Phe Asn Leu Asp Phe Pro Gln Asp Trp Gln Leu
 50 55 60

Tyr Gln Tyr His Val Thr Tyr Ile Pro Asp Leu Ala Ser Arg Arg Leu
 65 70 75 80

Arg Ile Ala Leu Leu Tyr Ser His Ser Glu Leu Ser Asn Lys Ala Lys
 85 90 95

Ala Phe Asp Gly Ala Ile Leu Phe Leu Ser Gln Lys Leu Glu Glu Lys
 100 105 110

Val Thr Glu Leu Ser Ser Glu Thr Gln Arg Gly Glu Thr Ile Lys Met
 115 120 125

Thr	Ile	Thr	Leu	Lys	Arg	Glu	Leu	Pro	Ser	Ser	Ser	Pro	Val	Cys	Ile	130	135	140
Gln	Val	Phe	Asn	Ile	Ile	Phe	Arg	Lys	Ile	Leu	Lys	Lys	Leu	Ser	Met	145	150	155
Tyr	Gln	Ile	Gly	Arg	Asn	Phe	Tyr	Asn	Pro	Ser	Glu	Pro	Met	Glu	Ile	165	170	175
Pro	Gln	His	Lys	Leu	Ser	Leu	Trp	Pro	Gly	Phe	Ala	Ile	Ser	Val	Ser	180	185	190
Tyr	Phe	Glu	Arg	Lys	Leu	Leu	Phe	Ser	Ala	Asp	Val	Ser	Tyr	Lys	Val	195	200	205
Leu	Arg	Asn	Glu	Thr	Val	Leu	Glu	Phe	Met	Thr	Ala	Leu	Cys	Gln	Arg	210	215	220
Thr	Gly	Leu	Ser	Cys	Phe	Thr	Gln	Thr	Cys	Glu	Lys	Gln	Leu	Ile	Gly	225	230	235
Leu	Ile	Val	Leu	Thr	Arg	Tyr	Asn	Asn	Arg	Thr	Tyr	Ser	Ile	Asp	Asp	245	250	255
Ile	Asp	Trp	Ser	Val	Lys	Pro	Thr	His	Thr	Phe	Gln	Lys	Arg	Asp	Gly	260	265	270
Thr	Glu	Ile	Thr	Tyr	Val	Asp	Tyr	Tyr	Lys	Gln	Gln	Tyr	Asp	Ile	Thr	275	280	285
Val	Ser	Asp	Leu	Asn	Gln	Pro	Met	Leu	Val	Ser	Leu	Leu	Lys	Lys	Lys	290	295	300
Arg	Asn	Asp	Asn	Ser	Glu	Ala	Gln	Leu	Ala	His	Leu	Ile	Pro	Glu	Leu	305	310	315
Cys	Phe	Leu	Thr	Gly	Leu	Thr	Asp	Gln	Ala	Thr	Ser	Asp	Phe	Gln	Leu	325	330	335
Met	Lys	Ala	Val	Ala	Glu	Lys	Thr	Arg	Leu	Ser	Pro	Ser	Gly	Arg	Gln	340	345	350

Gln Arg Leu Ala Arg Leu Val Asp Asn Ile Gln Arg Asn Thr Asn Ala
 355 360 365

Arg Phe Glu Leu Glu Thr Trp Gly Leu His Phe Gly Ser Gln Ile Ser
 370 375 380

Leu Thr Gly Arg Ile Val Pro Ser Glu Lys Ile Leu Met Gln Asp His
 385 390 395 400

Ile Cys Gln Pro Val Ser Ala Ala Asp Trp Ser Lys Asp Ile Arg Thr
 405 410 415

Cys Lys Ile Leu Asn Ala Gln Ser Leu Asn Thr Trp Leu Ile Leu Cys
 420 425 430

Ser Asp Arg Thr Glu Tyr Val Ala Glu Ser Phe Leu Asn Cys Leu Arg
 435 440 445

Arg Val Ala Gly Ser Met Gly Phe Asn Val Met Cys Ile Leu Pro Ser
 450 455 460

Asn Gln Lys Thr Tyr Tyr Asp Ser Ile Lys Lys Tyr Leu Ser Ser Asp
 465 470 475 480

Cys Pro Val Pro Ser Gln Cys Val Leu Ala Arg Thr Leu Asn Lys Gln
 485 490 495

Gly Met Met Met Ser Ile Ala Thr Lys Ile Ala Met Gln Met Thr Cys
 500 505 510

Lys Leu Gly Gly Glu Leu Trp Ala Val Glu Ile Pro Leu Lys Ser Leu
 515 520 525

Met Val Val Gly Ile Asp Val Cys Lys Asp Ala Leu Ser Lys Asp Val
 530 535 540

Met Val Val Gly Cys Val Ala Ser Val Asn Pro Arg Ile Thr Arg Trp
 545 550 555 560

Phe Ser Arg Cys Ile Leu Gln Arg Thr Met Thr Asp Val Ala Asp Cys
 565 570 575

Leu Lys Val Phe Met Thr Gly Ala Leu Asn Lys Trp Tyr Lys Tyr Asn
580 585 590

His Asp Leu Pro Ala Arg Ile Ile Val Tyr Arg Ala Gly Val Gly Asp
595 600 605

Gly Gln Leu Lys Thr Leu Ile Glu Tyr Glu Val Pro Gln Leu Leu Ser
610 615 620

Ser Val Ala Glu Ser Ser Ser Asn Thr Ser Ser Arg Leu Ser Val Ile
625 630 635 640

Val Val Arg Lys Lys Cys Met Pro Arg Phe Phe Thr Glu Met Asn Arg
645 650 655

Thr Val Gln Asn Pro Pro Leu Gly Thr Val Val Asp Ser Glu Ala Thr
660 665 670

Arg Asn Glu Trp Gln Tyr Asp Phe Tyr Leu Ile Ser Gln Val Ala Cys
675 680 685

Arg Gly Thr Val Ser Pro Thr Tyr Tyr Asn Val Ile Tyr Asp Asp Asn
690 695 700

Gly Leu Lys Pro Asp His Met Gln Arg Leu Thr Phe Lys Leu Cys His
705 710 715 720

Leu Tyr Tyr Asn Trp Pro Gly Ile Val Ser Val Pro Ala Pro Cys Gln
725 730 735

Tyr Ala His Lys Leu Thr Phe Leu Val Ala Gln Ser Ile His Lys Glu
740 745 750

Pro Ser Leu Glu Leu Ala Asn His Leu Phe Tyr Leu
755 760

<210> 73
<211> 861
<212> PRT
<213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> HIWI, predicted protein sequence

<400> 73

Met	Thr	Gly	Arg	Ala	Arg	Ala	Arg	Ala	Arg	Gly	Arg	Ala	Arg	Gly	Gln	1	5	10	15
Glu	Thr	Ala	Gln	Leu	Val	Gly	Ser	Thr	Ala	Ser	Gln	Gln	Pro	Gly	Tyr	20	25	30	
Ile	Gln	Pro	Arg	Pro	Gln	Pro	Pro	Pro	Ala	Glu	Gly	Glu	Leu	Phe	Gly	35	40	45	
Arg	Gly	Arg	Gln	Arg	Gly	Thr	Ala	Gly	Gly	Thr	Ala	Lys	Ser	Gln	Gly	50	55	60	
Leu	Gln	Ile	Ser	Ala	Gly	Phe	Gln	Glu	Leu	Ser	Leu	Ala	Glu	Arg	Gly	65	70	75	80
Gly	Arg	Arg	Arg	Asp	Phe	His	Asp	Leu	Gly	Val	Asn	Thr	Arg	Gln	Asn	85	90	95	
Leu	Asp	His	Val	Lys	Glu	Ser	Lys	Thr	Gly	Ser	Ser	Gly	Ile	Ile	Val	100	105	110	
Arg	Leu	Ser	Thr	Asn	His	Phe	Arg	Leu	Thr	Ser	Arg	Pro	Gln	Trp	Ala	115	120	125	
Leu	Tyr	Gln	Tyr	His	Ile	Asp	Tyr	Asn	Pro	Leu	Met	Glu	Ala	Arg	Arg	130	135	140	
Leu	Arg	Ser	Ala	Leu	Leu	Phe	Gln	His	Glu	Asp	Leu	Ile	Gly	Lys	Cys	145	150	155	160
His	Ala	Phe	Asp	Gly	Thr	Ile	Leu	Phe	Leu	Pro	Lys	Arg	Leu	Gln	Gln	165	170	175	
Lys	Val	Thr	Glu	Val	Phe	Ser	Lys	Thr	Arg	Asn	Gly	Glu	Asp	Val	Arg	180	185	190	

Ile	Thr	Ile	Thr	Leu	Thr	Asn	Glu	Leu	Pro	Pro	Thr	Ser	Pro	Thr	Cys
		195					200					205			
Leu	Gln	Phe	Tyr	Asn	Ile	Ile	Phe	Arg	Arg	Leu	Leu	Lys	Ile	Met	Asn
	210					215					220				
Leu	Gln	Gln	Ile	Gly	Arg	Asn	Tyr	Tyr	Asn	Pro	Asn	Asp	Pro	Ile	Asp
225					230					235					240
Ile	Pro	Ser	His	Arg	Leu	Val	Ile	Trp	Pro	Gly	Phe	Thr	Thr	Ser	Ile
				245					250					255	
Leu	Gln	Tyr	Glu	Asn	Ser	Ile	Met	Leu	Cys	Thr	Asp	Val	Ser	His	Lys
			260					265					270		
Val	Leu	Arg	Ser	Glu	Thr	Val	Leu	Asp	Phe	Met	Phe	Asn	Phe	Tyr	His
		275					280					285			
Gln	Thr	Glu	Glu	His	Lys	Phe	Gln	Glu	Gln	Val	Ser	Lys	Glu	Leu	Ile
	290					295					300				
Gly	Leu	Val	Val	Leu	Thr	Lys	Tyr	Asn	Asn	Lys	Thr	Tyr	Arg	Val	Asp
305					310					315					320
Asp	Ile	Asp	Trp	Asp	Gln	Asn	Pro	Lys	Ser	Thr	Phe	Lys	Lys	Ala	Asp
				325					330					335	
Gly	Ser	Glu	Val	Ser	Phe	Leu	Glu	Tyr	Tyr	Arg	Lys	Gln	Tyr	Asn	Gln
			340					345					350		
Glu	Ile	Thr	Asp	Leu	Lys	Gln	Pro	Val	Leu	Val	Ser	Gln	Pro	Lys	Arg
		355					360					365			
Arg	Arg	Gly	Pro	Gly	Gly	Thr	Leu	Pro	Gly	Pro	Ala	Met	Leu	Ile	Pro
	370					375					380				
Glu	Leu	Cys	Tyr	Leu	Thr	Gly	Leu	Thr	Asp	Lys	Met	Arg	Asn	Asp	Phe
385					390					395					400
Asn	Val	Met	Lys	Asp	Leu	Ala	Val	His	Thr	Arg	Leu	Thr	Pro	Glu	Gln
				405					410					415	

Arg	Gln	Arg	Glu	Val	Gly	Arg	Leu	Ile	Asp	Tyr	Ile	His	Lys	Asn	Asp	
			420					425					430			
Asn	Val	Gln	Arg	Glu	Leu	Arg	Asp	Trp	Gly	Leu	Ser	Phe	Asp	Ser	Asn	
		435					440					445				
Leu	Leu	Ser	Phe	Ser	Gly	Arg	Ile	Leu	Gln	Thr	Glu	Lys	Ile	His	Gln	
	450					455					460					
Gly	Gly	Lys	Thr	Phe	Asp	Tyr	Asn	Pro	Gln	Phe	Ala	Asp	Trp	Ser	Lys	
465					470					475					480	
Glu	Thr	Arg	Gly	Ala	Pro	Leu	Ile	Ser	Val	Lys	Pro	Leu	Asp	Asn	Trp	
				485					490					495		
Leu	Leu	Ile	Tyr	Thr	Arg	Arg	Asn	Tyr	Glu	Ala	Ala	Asn	Ser	Leu	Ile	
			500					505					510			
Gln	Asn	Leu	Phe	Lys	Val	Thr	Pro	Ala	Met	Gly	Met	Gln	Met	Arg	Lys	
		515					520					525				
Ala	Ile	Met	Ile	Glu	Val	Asp	Asp	Arg	Thr	Glu	Ala	Tyr	Leu	Arg	Val	
	530					535					540					
Leu	Gln	Gln	Lys	Val	Thr	Ala	Asp	Thr	Gln	Ile	Val	Val	Cys	Leu	Leu	
545					550					555					560	
Ser	Ser	Asn	Arg	Lys	Asp	Lys	Tyr	Asp	Ala	Ile	Lys	Lys	Tyr	Leu	Cys	
				565					570					575		
Thr	Asp	Cys	Pro	Thr	Pro	Ser	Gln	Cys	Val	Val	Ala	Arg	Thr	Leu	Gly	
			580					585					590			
Lys	Gln	Gln	Thr	Val	Met	Ala	Ile	Ala	Thr	Lys	Ile	Ala	Leu	Gln	Met	
		595					600					605				
Asn	Cys	Lys	Met	Gly	Gly	Glu	Leu	Trp	Arg	Val	Asp	Ile	Pro	Leu	Lys	
	610					615					620					
Leu	Val	Met	Ile	Val	Gly	Ile	Asp	Cys	Tyr	His	Asp	Met	Thr	Ala	Gly	
625					630					635					640	

Arg Arg Ser Ile Ala Gly Phe Val Ala Ser Ile Asn Glu Gly Met Thr
 645 650 655

Arg Trp Phe Ser Arg Cys Ile Phe Gln Asp Arg Gly Gln Glu Leu Val
 660 665 670

Asp Gly Leu Lys Val Cys Leu Gln Ala Ala Leu Arg Ala Trp Asn Ser
 675 680 685

Cys Asn Glu Tyr Met Pro Ser Arg Ile Ile Val Tyr Arg Asp Gly Val
 690 695 700

Gly Asp Gly Gln Leu Lys Thr Leu Val Asn Tyr Glu Val Pro Gln Phe
 705 710 715 720

Leu Asp Cys Leu Lys Ser Ile Gly Arg Gly Tyr Asn Pro Arg Leu Thr
 725 730 735

Val Ile Val Val Lys Lys Arg Val Asn Thr Arg Phe Phe Ala Gln Ser
 740 745 750

Gly Gly Arg Leu Gln Asn Pro Leu Pro Gly Thr Val Ile Asp Val Glu
 755 760 765

Val Thr Arg Pro Glu Trp Tyr Asp Phe Phe Ile Val Ser Gln Ala Val
 770 775 780

Arg Ser Gly Ser Val Ser Pro Thr His Tyr Asn Val Ile Tyr Asp Asn
 785 790 795 800

Ser Gly Leu Lys Pro Asp His Ile Gln Arg Leu Thr Tyr Lys Leu Cys
 805 810 815

His Ile Tyr Tyr Asn Trp Pro Gly Val Ile Arg Val Pro Ala Pro Cys
 820 825 830

Gln Tyr Ala His Lys Leu Ala Phe Leu Val Gly Gln Ser Ile His Arg
 835 840 845

Glu Pro Asn Leu Ser Leu Ser Asn Arg Leu Tyr Tyr Leu

<210> 74
 <211> 2571
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> eIF2C1, cDNA sequence of predicted ORF

<400> 74
 atggaagcgg gaccctcggg agcagctgcg ggcgcttacc tgccccccct gcagcaggtg 60
 ttccaggcac ctgcgccggc tggcattggc actgtgggga aaccaatcaa gtccttggcc 120
 aattactttg aggtggacat ccctaagatc gacgtgtacc actacgaggt ggacatcaag 180
 ccggataagt gtccccgtag agtcaaccgg gaagtggtag aatacatggg ccagcatttc 240
 aagcctcaga tcttttggtga tgcgaagcct gtgtatgatg gaaagaagaa catttacact 300
 gtcacagcac tgcccattgg caacgaacgg gtcgactttg aggtgacaat ccctggggaa 360
 gggaaggatc gaatctttaa ggtctccatc aagtggctag ccattgtgag ctggcgaatg 420
 ctgcatgagg ccctgggtcag cggccagatc cctgttcctt tggagtctgt gcaagccctg 480
 gatgtggcca tgaggcacct ggcattccatg aggtacaccc ctgtgggccg ctcttcttc 540
 tcaccgcctg agggctacta ccaccgcgtg ggggggtgggc gcgaggtctg gttcggcttt 600
 caccagtctg tgcgccctgc catgtggaag atgatgctca acattgatgt ctcagccact 660
 gccttttata aggcacagcc agtgattgag ttcattgtgt aggtgctgga catcaggaac 720
 atagatgagc agcccaagcc cctcacggac tctcagcgcg ttcgcttcac caaggagatc 780
 aagggcctga aggtggaagt caccactgt ggacagatga agaggaagta ccgcgtgtgt 840
 aatgttacct gtcgccctgc tagccatcag acattcccct tacagctgga gagtggacag 900
 actgtggagt gcacagtggc acagtatttc aagcagaaat ataaccttca gctcaagtat 960
 ccccatctgc cctgcctaca agttggccag gaacaaaagc atacctacct tcccctagag 1020
 gtctgtaaca ttgtggctgg gcagcgctgt attaaaaagc tgaccgacaa ccagacctcg 1080
 accatgataa aggccacagc tagatccgct ccagacagac aggaggagat cagtcgcctg 1140
 atgaagaatg ccagctacaa cttagatccc tacatccagg aatttgggat caaagtgaag 1200
 gatgacatga cggaggtgac agggcgagtg ctgccggcgc ccatcttgca gtacggcggc 1260

cggaaccggg	ccattgccac	acccaatcag	ggtgtctggg	acatgcgggg	gaaacagttc	1320
tacaatggga	ttgagatcaa	agtctggggc	atcgcttgct	tcgcacccca	aaaacagtgt	1380
cgagaagagg	tgctcaagaa	cttcacagac	cagctgcgga	agatttccaa	ggatgcgggg	1440
atgcctatcc	aggggtcaacc	ttgtttctgc	aaatatgcac	agggggcaga	cagcgtggag	1500
cctatgttcc	ggcatctcaa	gaacacctac	tcagggctgc	agctcattat	tgtcatcctg	1560
ccaggggaaga	cgccggtgta	tgctgaggtg	aaacgtgtcg	gagatacact	cttggggaatg	1620
gctacgcagt	gtgtgcaggt	gaagaacgtg	gtcaagacct	cacctcagac	tctgtccaac	1680
ctctgcctca	agatcaatgt	caaacttggt	ggcattaaca	acatcctagt	cccacaccag	1740
cgctctgccg	tttttcaaca	gccagtgata	ttcctgggag	cagatgttac	acacccccca	1800
gcaggggatg	ggaaaaaacc	ttctatcaca	gcagtggtag	gcagtatgga	tgcccacccc	1860
agccgatact	gtgctactgt	gcgggtacag	cgaccacggc	aagagatcat	tgaagacttg	1920
tcctacatgg	tgcgtagagct	cctcatccaa	ttctacaagt	ccaccgttt	caagcctacc	1980
cgcatcatct	tctaccgaga	tggggtgcct	gaaggccagc	tacccagat	actccactat	2040
gagctactgg	ccattcgtga	tgcttgcac	aaactggaaa	aggactacca	gcctgggatc	2100
acttatattg	tggtgcagaa	acgccatcac	acccgccttt	tctgtgctga	caagaatgag	2160
cgaattggga	agagtggtaa	catcccagct	gggaccacag	tggacaccaa	catcacccac	2220
ccatttgagt	ttgacttcta	tctgtgcagc	cacgcaggca	tccagggcac	cagccgacca	2280
tcccattact	atgttctttg	ggatgacaac	cgtttcacag	cagatgagct	ccagatcctg	2340
acgtaccagc	tgtgccacac	ttacgtacga	tgcacacgct	ctgtctctat	cccagcacct	2400
gcctactatg	cccgcttggg	ggctttccgg	gcacgatacc	acctggtgga	caaggagcat	2460
gacagtggag	aggggagcca	catatcgggg	cagagcaatg	ggcgggaccc	ccaggccctg	2520
gccaaagccg	tgacaggttca	ccaggatact	ctgcgcacca	tgtacttcgc	t	2571

<210> 75
 <211> 2580
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> eIF2C2, cDNA sequence of predicted ORF

<400> 75

atgggtgttc	tctctgccat	tcccgcactt	gcacctcctg	cgccgcccgc	ccccatccaa	60
ggatatgcct	tcaagcctcc	acctagaccc	gactttggga	cctccgggag	aacaatcaaa	120
ttacaggcca	atttcttcga	aatggacatc	cccaaaattg	acatctatca	ttatgaattg	180
gatatcaagc	cagagaagtg	cccgaggaga	gttaacaggg	aaatcgtgga	acacatggtc	240
cagcacttta	aaacacagat	ctttggggat	cggaagcccg	tgtttgacgg	caggaagaat	300
ctatacacag	ccatgcccct	tccgattggg	agggacaagg	tggagctgga	ggtcacgctg	360
ccaggagaag	gcaaggatcg	catcttcaag	gtgtccatca	agtgggtgtc	ctgcgtgagc	420
ttgcaggcgt	tacacgatgc	actttcaggg	cggctgccc	gcgtcccttt	tgagacgatc	480
caggccctgg	acgtgggtcat	gaggcacttg	ccatccatga	ggtagacccc	cgtgggcccgc	540
tccttcttca	ccgcgtccga	aggctgctct	aaccctcttg	gcgggggccc	agaagtgtgg	600
tttggcttcc	atcagtcctg	ccggccttct	ctctggaaaa	tgatgctgaa	tattgatgtg	660
tcagcaacag	cgttttacaa	ggcacagcca	gtaatcgagt	ttgtttgtga	agttttggat	720
tttaaaagta	ttgaagaaca	acaaaaacct	ctgacagatt	cccaaagggg	aaagtttacc	780
aaagaaatta	aaggtctaaa	ggtggagata	acgcactgtg	ggcagatgaa	gaggaagtac	840
cgtgtctgca	atgtgacccg	gcggcccgc	agtcaccaaa	cattcccgtc	gcagcaggag	900
agcgggcaga	cggtggagtg	cacggtggcc	cagtatttca	aggacaggca	caagttggtt	960
ctgcgctacc	cccacctccc	atgtttacaa	gtcggacagg	agcagaaaca	cacctacctt	1020
cccctggagg	tctgtaacat	tgtggcagga	caaagatgta	ttaaaaaatt	aacggacaat	1080
cagacctcaa	ccatgatcag	agcaactgct	aggtcggcgc	ccgatcggca	agaagagatt	1140
agcaaattga	tgcgaagtgc	aagtttcaac	acagatccat	acgtccgtga	atttggaatc	1200
atgggtcaaag	atgagatgac	agacgtgact	gggcgggtgc	tgagccgc	ctccatcctc	1260
tacgggggca	ggaataaagc	tattgcgacc	cctgtccagg	gcgtctggga	catgcggaac	1320
aagcagttcc	acacgggcat	cgagatcaag	gtgtgggcca	ttgcgtgctt	cgccccccag	1380
cgccagtgca	cggaagtcca	tctgaagtcc	ttcacagagc	agtcagaaa	gatctcgaga	1440
gacgtggca	tgcccatcca	gggccagccg	tgcttctgca	aatacgcgca	gggggcggac	1500
agcgtggagc	ccatgttccg	gcacctgaag	aacacgtatg	cgggcctgca	gctggtggtg	1560
gtcatcctgc	ccggcaagac	gcccggtgtac	gccgaggtca	agcgcgtggg	agacacggtg	1620

ctgggggatgg ccacgcagtg cgtgcagatg aagaacgtgc agaggaccac gccacagacc	1680
ctgtccaacc tttgcctgaa gatcaacgtc aagctgggag gcgtgaacaa catcctgctg	1740
ccccagggca ggccgccggt gttccagcag cccgtcatct ttctgggagc agacgtcact	1800
cacccccccg ccgggggatgg gaagaagccc tccattgccg ccgtggtggg cagcatggac	1860
gccaccccca atcgctactg cgccaccgtg cgcgtgcagc agcaccggca ggagatcata	1920
caagacctgg ccgccatggt ccgcgagctc ctcatccagt tctacaagtc cacgcgcttc	1980
aagcccaccc gcatcatctt ctaccgcgac ggtgtctctg aaggccagtt ccagcaggtt	2040
ctccaccacg agttgctggc catccgtgag gcctgtatca agctagaaaa agactaccag	2100
cccgggatca ccttcatcgt ggtgcagaag aggcaccaca cccggctctt ctgcactgac	2160
aagaacgagc ggggttgggaa aagtggaaac attccagcag gcacgactgt ggacacgaaa	2220
atcacccacc ccaccgagtt cgacttctac ctgtgtagtc acgctggcat ccaggggaca	2280
agcaggcctt cgcactatca cgtcctctgg gacgacaatc gtttctctc tgatgagctg	2340
cagatcctaa cctaccagct gtgtcacacc tacgtgcgct gcacacgctc cgtgtccatc	2400
ccagcgccag catactacgc tcacctggtg gccttccggg ccaggtacca cctggtggat	2460
aaggaacatg acagtgtga aggaagccat acctctgggc agagtaacgg gcgagaccac	2520
caagcactgg ccaaggcggt ccaggttcac caagacactc tgcgcaccat gtactttgct	2580

<210> 76
 <211> 2772
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> eIF2C3, cDNA sequence of predicted ORF

<400> 76	
agccggagcc gggtccttgt ccccgggccg ggcgccgccc ccgccccctg cccagcgccc	60
gcgtctccgc ggcgccaccc cagcgccaat attccggaga tcaagcgta cgcggcggcg	120
gcggcggcgg cggcgggggc cggagcggga ggcgccgggg accggggcga ggcggccccc	180
gccgcccga tggaggcgct gggaccggga cctccggcta gcctgtttca gccacctcgt	240
cgtcctggcc ttggaactgt tggaaaacca attcgactgt tagccaatca ttttcaggtt	300

cagattccta	aaatagatgt	gtatcactat	gatgtggata	ttaagcctga	aaaacggcct	360
cgtagagtca	acagggaggt	agtagataca	atggtgcggc	acttcaagat	gcaaataattt	420
ggtgatcggc	agcctgggta	tgatggcaaa	agaaacatgt	acacagcaca	tccactacca	480
attggacggg	ataggggttg	tatggaggtg	actcttcag	gcgagggtaa	agaccaaaca	540
tttaaagtgt	ctgttcagt	ggtgtcagtt	gtgagccttc	agttgctttt	agaagctttg	600
gctgggcact	tgaatgaagt	cccagatgac	tcagtacaag	cacttgatgt	tatcacaaga	660
caccttcct	ccatgaggt	caccccagtg	ggcggttcct	ttttctcacc	cccggaaggt	720
tactaccacc	ctctgggagg	gggcaggag	gtctggtttg	gttttcatca	gtctgtgaga	780
cctgccatgt	ggaatatgat	gctcaacatt	gatgtatctg	caactgcttt	ctaccgggct	840
cagcctatca	ttgagttcat	gtgtgaggtt	ttagacattc	agaacatcaa	tgaacagacc	900
aaacctctaa	cagactccca	gcgtgtcaaa	tttaccaaag	aatcagagg	tctcaaagtt	960
gaggtgaccc	actgtggaca	gatgaaacga	aaataccgag	tttgtaatgt	gactagacgg	1020
ccagccagtc	atcaaacttt	tcctttgcag	ctagaaaacg	gtcaagctat	ggaatgtaca	1080
gtagctcaat	attttaagca	aaagtatagt	ctgcaactga	aataccccca	tcttccctgt	1140
ctccaagtgg	gacaagaaca	aaagcataca	tacttgccac	tcgaggctctg	taatatagtg	1200
gcaggacagc	gatgtatcaa	gaagctcaca	gacaatcaga	cttcacaaat	gatcaaagct	1260
acagcaagat	ctgctcctga	cagacaggaa	gagatcagta	gactgggtgaa	gagcaacagt	1320
atggtgggtg	gacctgatcc	ataccttaaa	gaatttggt	ttgttgtcca	caatgaaatg	1380
acagagctca	caggcagggt	acttcagca	ccaatgctgc	aatatggagg	ccggaataaa	1440
acagtagcca	cacccaacca	gggtgtctgg	gacatgcgag	gaaagcagtt	ttatgctggc	1500
attgaaatta	aagtttgggc	agttgcttgt	tttgcacctc	agaaacaatg	tagggaagat	1560
ttactaaaga	gtttcactga	ccagctgcgt	aaaatctcta	aggatgcagg	aatgcccctc	1620
cagggtcagc	catgtttctg	caagtatgca	caagggtgcag	acagtgtgga	gcctatgttt	1680
aaacatctga	aatgactta	tgtgggccta	cagctaatag	tggttatcct	gcctggaaag	1740
acaccagtat	atgcggaggt	gaaacgtgtt	ggagataccc	ttctaggtat	ggccacacag	1800
tgtgtccagg	taaaaaatgt	agtgaagacc	tcacctcaaa	ccctttccaa	tctttgcttg	1860
aagataaatg	caaaacttgg	aggaattaac	aatgtgcttg	tgctcatca	aaggccctcg	1920
gtgttccagc	agcctgtcat	cttctggga	gcggatgtca	cacaccccc	agcaggggat	1980

gggaagaaac cttccattgc tgctgtggtt ggcagtatgg atggccaccc cagccggtac	2040
tgtgccaccg ttcgggtgca gacttcccgg caggagatct cccaagagct cctctacagt	2100
caagagggtca tccaggacct gactaacatg gttcgagagc tgctgattca gttctacaaa	2160
tccacacgct tcaaaccac tcggatcatc tattaccgtg gaggggtatc tgagggacaa	2220
atgaaacagg tagcttggcc agaactaata gcaattcgaa aggcattgtat tagcttggaa	2280
gaagattacc ggccaggaat aacttatatt gtggtgcaaa aaagacatca cacacgactc	2340
ttctgtgcag ataaaacaga aagggtaggg aaaagtggca atgtaccagc aggcactaca	2400
gtggatagta ccatcacaca tccatctgag tttgactttt acctctgtag tcatgcagga	2460
attcagggaa ccagccgtcc ctcacattac caggtcttgt gggatgacaa ctgcttcact	2520
gcagatgaac tccagctact gacttaccag ctgtgtcaca cctatgtgag gtgcactcgc	2580
tcagtctcta ttccagcccc tgcataattat gcccggttg tagcatttag ggcaaggtag	2640
catctggtgg ataaagatca tgacagtgcg gaaggcagtc atgtgtcagg acagagcaac	2700
ggccgggatc ctcaggcctt ggctaaggct gtgcaaatcc accatgatac ccagcacacg	2760
atgtattttg cc	2772

<210> 77
 <211> 2568
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> eIF2C4, cDNA sequence of predicted ORF

<400> 77	
gcaggaccgc ctggggccca gccctactc atggtgccca gaagacctgg ctatggcacc	60
atgggcaaac ccattaaact gctggctaac tgttttcaag ttgaaatccc aaagattgat	120
gtctacctct atgaggtaga tattaacca gacaagtgtc ctaggagagt gaacagggag	180
gtggttgact caatggttca gcattttaaa gtaactatat ttggagaccg tagaccagtt	240
tatgatggaa aaagaagtct ttacaccgcc aatccacttc ctgtggcaac tacaggggta	300
gatttagacg ttactttacc tggggaagggt ggaaaagatc gacctttcaa ggtgtcaatc	360
aaatttgtct ctcggtgtag ttggcaccta ctgcatgaag tactgacagg acggaccttg	420

cctgagccac	tggaattaga	caagccaatc	agcactaacc	ctgtccatgc	cgttgatgtg	480
gtgctacgac	atctgccctc	catgaaatac	acacctgtgg	ggcgttcatt	tttctccgct	540
ccagaaggat	atgaccaccc	tctggggagg	ggcagggaag	tgtggtttgg	attccatcag	600
tctgttcggc	ctgccatgtg	gaaaatgatg	cttaatatcg	atgtttctgc	cactgccttc	660
tacaaagcac	aacctgtaat	tcagttcatg	tgtgaagtgc	ttgatattca	taatattgat	720
gagcaaccaa	gacctctgac	tgattctcat	cgggtaaaat	tcaccaaaga	gataaaagg	780
ttgaagggtg	aagtgactca	ttgtggaaca	atgagacgga	aataccgtgt	ttgtaatgta	840
acaaggaggc	ctgccagtca	tcaaaccctt	cctttacagt	tagaaaacgg	ccaaactgtg	900
gagagaacag	tagcgcagta	tttcagagaa	aagtatactc	ttcagctgaa	gtacccgcac	960
cttcctctgc	tgcaagtcgg	gcaggaacag	aaacacacct	acctgccact	agaagtctgt	1020
aatattgtgg	cagggcaacg	atgtatcaag	aagctaacag	acaatcagac	ttccactatg	1080
atcaaggcaa	cagcaagatc	tgcaccagat	agacaagagg	aaattagcag	attggtaaga	1140
agtgcaaatt	atgaaacaga	tccatttggt	caggagtttc	aatttaaagt	tcgggatgaa	1200
atggctcatg	taactggacg	cgtacttcca	gcacctatgc	tccagtatgg	aggacggaat	1260
cggacagtag	caacaccgag	ccatggagta	tgggacatgc	gagggaacaa	attccacaca	1320
ggagttgaaa	tcaaaatgtg	ggctatcgct	tgttttgcca	cacagaggca	gtgcagagaa	1380
gaaatattga	agggtttcac	agaccagctg	cgtaagattt	ctaaggatgc	agggatgccc	1440
atccagggcc	agccatgctt	ctgcaaatat	gcacaggggg	cagacagcgt	agagcccatg	1500
ttccggcatc	tcaagaacac	atattctggc	ctacagctta	ttatcgatc	cctgccgggg	1560
aagacaccag	tgtatgcgga	agtgaacagt	gtaggagaca	cacttttggg	tatggctaca	1620
caatgtgttc	aagtcaagaa	tgtaataaaa	acatctcttc	aaactctgtc	aaacttgtgc	1680
ctaaagataa	atgttaaact	cggagggatc	aataatattc	ttgtacctca	tcaaagacct	1740
tctgtgttcc	agcaaccagt	gatctttttg	ggagccgatg	tcactcatcc	acctgctggt	1800
gatggaaaga	agccttctat	tgctgctgtt	gtaggtagta	tggatgcaca	ccaagcaga	1860
tactgtgcca	cagtaagagt	tcagagaccc	cgacaggaga	tcattccagga	cttggcctcc	1920
atgggtccgg	aacttcttat	tcaattttat	aagtcaactc	ggttcaagcc	tactcgtatc	1980
atcttttatc	gggatggtgt	ttcagagggg	cagtttaggc	aggtattata	ttatgaacta	2040
ctagcaattc	gagaagcctg	catcagtttg	gagaaagact	atcaacctgg	aataacctac	2100

attgtagttc agaagagaca tcacactcga ttatTTTgtg ctgataggac agaaagggtt	2160
ggaagaagtg gcaatatccc agctggaaca acagttgata cagacattac acacccatat	2220
gagttcgatt tttacctctg tagccatgct ggaatacagg gtaccagtcg tccttcacac	2280
tatcatgttt tatgggatga taactgcttt actgcagatg aacttcagct gctaacttac	2340
cagctctgcc acacttacgt acgctgtaca cgatctgttt ctatacctgc accagcgtat	2400
tatgctcacc tggtagcatt tagagccaga tatcatcttg tggacaaaga acatgacagt	2460
gctgaaggaa gtcacgtttc aggacaaagc aatgggagag atccacaagc tcttgccaag	2520
gctgtacaga ttcaccaaga taccttacgc acaatgtact tcgcttaa	2568

<210> 78
 <211> 2292
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> HILI, cDNA sequence of predicted ORF

<400> 78	
atatcttctg gtgatgctgg agtaccttc atggaaagag gtgtgaaaaa caaacaggac	60
tttatggatt tgagtatctg taccagagaa aaattggcac atgtgagaaa ttgtaaaaca	120
ggttccagtg gaatacctgt gaaactgggtt acaaacctct ttaacttaga ttttcccaa	180
gactggcagc tataccagta ccatgtgaca tatattccag atttagcatc tagaaggctg	240
agaattgctt tactttatag tcatagtga ctttccaaca aagcaaaagc attcgacggt	300
gccatccttt ttctgtcaca aaagctagaa gaaaagggtca cagagttgtc aagtgaaact	360
caaagagggtg agactataaa gatgactatc accctgaaga gggagctgcc atcaagttct	420
cccgtgtgca tccaggctct caatatcatc ttcagaaaga tcctcaaaaa gttgtccatg	480
taccaaattg gacggaactt ctataatcct tcagagccaa tggaaattcc ccagcacaaa	540
ttatcccttt ggccctgggtt tgccatttct gtgtcatatt ttgaaaggaa gctcctgttt	600
agtgtgatg tgagttacaa agtcctccgg aatgagacgg ttctggaatt catgactgct	660
ctctgtcaaa gaactggctt gtcctgtttc acccagacgt gtgagaagca gctaataggg	720
ctcattgtcc ttacaagata caataacaga acctactcca ttgatgacat tgactgggtca	780

gtgaagccca	cacacacctt	tcagaagcgg	gatggcaccg	agatcaccta	tgtggattac	840
tacaagcagc	agtatgatat	tactgtatcg	gacctgaatc	agcccatgct	tgttagtctg	900
ttaaagaaga	agagaaatga	caacagtgag	gctcagctcg	cccacctgat	acctgagctc	960
tgctttctaa	cagggctgac	tgaccaggca	acatctgatt	tccagctgat	gaaggctgtg	1020
gctgaaaaga	cacgtctcag	tccttcaggc	cggcagcagc	gcctggccag	gcttgtggac	1080
aacatccaga	ggaataccaa	tgctcgcttt	gaactagaga	cctggggact	gcatttttga	1140
agccagatat	ctctgactgg	ccggattgtg	ccttcagaaa	aaatattaat	gcaagaccac	1200
atatgtcaac	ctgtgtctgc	tgctgactgg	tccaaggata	ttcgaacttg	caagatttta	1260
aatgcacagt	ctttgaatac	ctggttgatt	ttatgtagcg	acagaactga	atatgttgcc	1320
gagagctttc	tgaactgctt	gagaagagtt	gcaggttcca	tgggatttaa	tgtaatgtgc	1380
attctgcctt	ctaatacaga	gacctattat	gattccatta	aaaaatattt	gagctcagac	1440
tgcccagtc	caagccaatg	tgtgcttgct	cggaccttga	ataaacaggg	catgatgatg	1500
agtatcgcca	ccaagatcgc	tatgcagatg	acttgcaagc	tccgaggcga	gctgtgggct	1560
gtggaaatac	ctttaaagtc	cctgatggtg	gtcgggtattg	atgtctgtaa	agatgcactc	1620
agcaaggacg	tgatggttgt	tggatgcgtg	gccagtgtta	acccagaat	caccagggtg	1680
ttttcccgct	gtatccttca	gagaacaatg	actgatgttg	cagattgctt	gaaagttttc	1740
atgactggag	cactcaacaa	atggtacaag	tacaatcatg	atttgccagc	acggataatt	1800
gtgtaccgtg	ctggtgtagg	ggatggtcag	ctgaaaacac	ttattgaata	tgaagtccca	1860
cagctgctga	gcagtgtggc	agaatccagc	tcaaatacca	gctcaagact	gtcggtgatt	1920
gtggtcagga	agaagtgcac	gccacgattc	tttaccgaaa	tgaaccgcac	tgtacagaac	1980
ccccacttg	gcactgttgt	ggattcagaa	gcaacacgta	acgaatggca	gtatgacttt	2040
tatctgatca	gccagggtgg	ctgccgggga	actgttagtc	ctacctacta	taatgtcatc	2100
tatgatgaca	acggcttgaa	gcccgaccat	atgcagagac	ttacattcaa	attgtgccac	2160
ctgtactaca	actggccggg	catagtcagt	gtcccagcac	catgtcagta	tgctcacaag	2220
ctgacctttc	tggtggcaca	aagcattcat	aaagaaccca	gtctggaatt	agccaaccat	2280
ctcttctacc	tg					2292

<210> 79
<211> 2583

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> HIWI, cDNA sequence of predicted ORF

<400> 79
atgactggga gagcccgagc cagagccaga ggaagggccc gcggtcagga gacagcgag 60
ctggtgggct ccactgccag tcagcaacct gggttatattc agcctaggcc tcagccgcca 120
ccagcagagg gggaattatt tggccgtgga cggcagagag gaacagcagg aggaacagcc 180
aagtcacaag gactccagat atctgctgga tttcaggagt tatcgttagc agagagagga 240
ggtcgtcgta gagattttca tgatcttggt gtgaatacaa ggcagaacct agaccatggt 300
aaagaatcaa aaacagggtt ttcaggcatt atagtaaggt taagcactaa ccatttccgg 360
ctgacatccc gtccccagtg ggccttatat cagtatcaca ttgactataa cccactgatg 420
gaagccagaa gactccgttc agctcttctt tttcaacacg aagatctaata tggaaagtgc 480
catgcttttg atggaacgat attattttta cctaaaagac tacagcaaaa ggttactgaa 540
gttttttagta agacccggaa tggagaggat gtgaggataa cgatcacttt aacaaatgaa 600
cttccaccta catcaccaac ttgtttgcag ttctataata ttattttcag gaggcttttg 660
aaaatcatga atttgcaaca aattggacga aattattata acccaaataga cccaattgat 720
attccaagtc acaggttggt gatttggcct ggcttcacta cttccatcct tcagtatgaa 780
aacagcatca tgctctgcac tgacgttagc cataaagtcc ttcgaagtga gactgttttg 840
gatttcatgt tcaactttta tcatcagaca gaagaacata aatttcaaga acaagtttcc 900
aaagaactaa taggtttagt tgttcttacc aagtataaca ataagacata cagagtggat 960
gatattgact gggaccagaa tccaagagc acctttaaga aagccgacgg ctctgaagtc 1020
agcttcttag aatactacag gaagcaatac aaccaagaga tcaccgactt gaagcagcct 1080
gtcttggtca gccagcccaa gagaaggcgg ggccctgggg ggacactgcc agggcctgcc 1140
atgctcattc ctgagctctg ctatcttaca ggtctaactg ataaaatgcg taatgatttt 1200
aacgtgatga aagacttagc cgttcataca agactaactc cagagcaaag gcagcgtgaa 1260
gtgggacgac tcattgatta cattcataaa aacgataatg ttcaaagga gcttcgagac 1320
tggggtttga gctttgattc caacttactg tccttctcag gaagaatttt gcaaacagaa 1380

aagattcacc aaggtggaaa aacatttgat tacaatccac aatttgcaga ttggtccaaa	1440
gaaacaagag gtgcaccatt aattagtgtt aagccactag ataactggct gttgatctat	1500
acgcgaagaa attatgaagc agccaattca ttgatacaaa atctatttaa agttacacca	1560
gccatgggca tgcaaagag aaaagcaata atgattgaag tggatgacag aactgaagcc	1620
tacttaagag tcttacagca aaaggtcaca gcagacaccc agatagttgt ctgtctgttg	1680
tcaagtaatc ggaaggacaa atacgatgct attaaaaaat acctgtgtac agattgccct	1740
accccaagtc agtgtgtggt ggcccgaacc ttaggcaaac agcaaactgt catggccatt	1800
gctacaaaga ttgccctaca gatgaactgc aagatgggag gagagctctg gaggggtggac	1860
atccccctga agctcgtgat gatcgttggc atcgattgtt accatgacat gacagctggg	1920
cggaggtcaa tcgcaggatt tgttgccagc atcaatgaag ggatgaccgc ctggttctca	1980
cgtgcatat ttcaggatag aggacaggag ctggtagatg ggctcaaagt ctgcctgcaa	2040
gcggctctga gggcttgga tagctgcaat gagtacatgc ccagccggat catcgtgtac	2100
cgcgatggcg taggagacgg ccagctgaaa aactggtga actacgaagt gccacagttt	2160
ttggattgtc taaaatccat tggtagaggt tacaacccta gactaacggt aattgtggtg	2220
aagaaaagag tgaacaccag attttttgct cagtctggag gaagacttca gaatccactt	2280
cctggaacag ttattgatgt agaggttacc agaccagaat ggtatgactt ttttatcgtg	2340
agccaggctg tgagaagtgg tagtgtttct cccacacatt acaatgtcat ctatgacaac	2400
agcggcctga agccagacca catacagcgc ttgacctaca agctgtgcca catctattac	2460
aactggccag gtgtcattcg tgttcctgct ccttgccagt acgcccacaa gctggctttt	2520
cttgttggcc agagtattca cagagagcca aatctgtcac tgtcaaaccg cttttactac	2580
ctc	2583

<210> 80
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligodeoxynucleotide with homology to human gene

<220>
 <221> misc_feature
 <223> eIF2C1, primer (5'-3')

<400> 80
 gaggtctgta acattgtggc 20

<210> 81
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligodeoxynucleotide with homology to human gene

<220>
 <221> misc_feature
 <223> eIF2C1, primer (5'-3')

<400> 81
 cggtagaaga tgatgcgggt 20

<210> 82
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligodeoxynucleotide with homology to human gene

<220>
 <221> misc_feature
 <223> eIF2C1, primer (5'-3')

<400> 82
 gaggtctgta acattgtggc 20

<210> 83
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligodeoxynucleotide with homology to human gene

<220>
 <221> misc_feature
 <223> eIF2C1, primer (5'-3')

<400> 83
 aagttcttga gcacctcttc tcga 24

<210> 84
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligodeoxynucleotide with homology to human gene

<220>
<221> misc_feature
<223> eIF2C1, primer (5'-3')

<400> 84
gaggtctgta acattgtggc

20

<210> 85
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligodeoxynucleotide with homology to human gene

<220>
<221> misc_feature
<223> eIF2C1, primer (5'-3')

<400> 85
cggtagaaga tgatgcgggt

20

<210> 86
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligodeoxynucleotide with homology to human gene

<220>
<221> misc_feature
<223> eIF2C1, primer (5'-3')

<400> 86
ccacaccagc gctctgcc

18

<210> 87
<211> 18
<212> DNA

<213> Artificial Sequence

<220>

<223> Oligodeoxynucleotide with homology to human gene

<220>

<221> misc_feature

<223> eIF2C1, primer (5'-3')

<400> 87

ctcacgcacc atgtagga

18

<210> 88

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligodeoxynucleotide with homology to human gene

<220>

<221> misc_feature

<223> eIF2C2, primer (5'-3')

<400> 88

gaggtctgta acattgtggc

20

<210> 89

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligodeoxynucleotide with homology to human gene

<220>

<221> misc_feature

<223> eIF2C2, primer (5'-3')

<400> 89

cggtagaaga tgatgcgggt

20

<210> 90

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligodeoxynucleotide with homology to human gene

<220>
<221> misc_feature
<223> eIF2C2, primer (5'-3')

<400> 90
atcctgctgc cccaaggg

18

<210> 91
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligodeoxynucleotide with homology to human gene

<220>
<221> misc_feature
<223> eIF2C2, primer (5'-3')

<400> 91
gatctcctgc cggtgctg

18

<210> 92
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> Oligodeoxynucleotide with homology to human gene

<220>
<221> misc_feature
<223> eIF2C2, primer (5'-3')

<400> 92
gaggtctgta acattgtggc

20

<210> 93
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligodeoxynucleotide with homology to human gene

<220>
<221> misc_feature
<223> eIF2C2, primer (5'-3')

<400> 93
cggtagaaga tgatgcgggt

20

<210> 94
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligodeoxynucleotide with homology to human gene

<220>
<221> misc_feature
<223> eIF2C2, primer (5'-3')

<400> 94
gaggtctgta acattgtggc

20

<210> 95
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligodeoxynucleotide with homology to human gene

<220>
<221> misc_feature
<223> eIF2C2, primer (5'-3')

<400> 95
gatctcctgc cgggtgctg

18

<210> 96
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligodeoxynucleotide with homology to human gene

<220>
<221> misc_feature
<223> eIF2C3, primer (5'-3')

<400> 96
agagcaacag tatgggtgggt ggac

24

<210> 97
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligodeoxynucleotide with homology to human gene

<220>
<221> misc_feature
<223> eIF2C3, primer (5'-3')

<400> 97
tggatgtgtg atggtact

18

<210> 98
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligodeoxynucleotide with homology to human gene

<220>
<221> misc_feature
<223> eIF2C3, primer (5'-3')

<400> 98
cctctacagt caagaggt

18

<210> 99
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligodeoxynucleotide with homology to human gene

<220>
<221> misc_feature
<223> eIF2C3, primer (5'-3')

<400> 99
tggatgtgtg atggtact

18

<210> 100
<211> 18
<212> DNA

<213> Artificial Sequence

<220>

<223> Oligodeoxynucleotide with homology to human gene

<220>

<221> misc_feature

<223> eIF2C3, primer (5'-3')

<400> 100

cacttgaatg aagtccca

18

<210> 101

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligodeoxynucleotide with homology to human gene

<220>

<221> misc_feature

<223> eIF2C3, primer (5'-3')

<400> 101

tcctggatga cctcttgact gtag

24

<210> 102

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligodeoxynucleotide with homology to human gene

<220>

<221> misc_feature

<223> eIF2C3, primer (5'-3')

<400> 102

agagcaacag tatggtgggt ggac

24

<210> 103

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligodeoxynucleotide with homology to human gene

<220>
<221> misc_feature
<223> eIF2C3, primer (5'-3')

<400> 103
tcctggatga cctcttgact gtag

24

<210> 104
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligodeoxynucleotide with homology to human gene

<220>
<221> misc_feature
<223> eIF2C4, primer (5'-3')

<400> 104
tccggcatct caagaacaca tattct

26

<210> 105
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligodeoxynucleotide with homology to human gene

<220>
<221> misc_feature
<223> eIF2C4, primer (5'-3')

<400> 105
gaactcatat ggggtgtgtaa tgtctg

26

<210> 106
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligodeoxynucleotide with homology to human gene

<220>
<221> misc_feature

<223> eIF2C4, primer (5'-3')

<400> 106

atccaggact tggcctcc

18

<210> 107

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligodeoxynucleotide with homology to human gene

<220>

<221> misc_feature

<223> eIF2C4, primer (5'-3')

<400> 107

gaactcatat ggggtgtgtaa tgtctg

26

<210> 108

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligodeoxynucleotide with homology to human gene

<220>

<221> misc_feature

<223> HILI, primer (5'-3')

<400> 108

cagcacaaat tatccctt

18

<210> 109

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligodeoxynucleotide with homology to human gene

<220>

<221> misc_feature

<223> HILI, primer (5'-3')

<400> 109

cggcctgaag gactgagacg tgt

23

<210> 110
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligodeoxynucleotide with homology to human gene

<220>
<221> misc_feature
<223> HILI, primer (5'-3')

<400> 110
cagcacaaat tatccctt

18

<210> 111
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligodeoxynucleotide with homology to human gene

<220>
<221> misc_feature
<223> HILI, primer (5'-3')

<400> 111
gtgtgtgggc ttcactga

18

<210> 112
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligodeoxynucleotide with homology to human gene

<220>
<221> misc_feature
<223> HILI, primer (5'-3')

<400> 112
tctctgtcaa agaactggct tgtcct

26

<210> 113
<211> 18

<212> DNA
<213> Artificial Sequence

<220>
<223> Oligodeoxynucleotide with homology to human gene

<220>
<221> misc_feature
<223> HILI, primer (5'-3')

<400> 113
ctgtacagtg cggttcat

18

<210> 114
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligodeoxynucleotide with homology to human gene

<220>
<221> misc_feature
<223> HILI, primer (5'-3')

<400> 114
tctctgtcaa agaactggct tgcct

26

<210> 115
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligodeoxynucleotide with homology to human gene

<220>
<221> misc_feature
<223> HILI, primer (5'-3')

<400> 115
cggcctgaag gactgagacg tgt

23